AMENDMENTS TO THE SPECIFICATIONS:

Please replace paragraph RELATED APPLICATIONS on page 2 with the following amended paragraph:

This application is related to U.S. Patent Application Serial Number 09/721,042 filed on November 21,2000, entitled "Methods and Computer Software Products for predicting Nucleic Acid Hybridization Affinity"; U.S. Patent Application Serial Number 09/718,295, filed November 21, 2000, entitled "Methods and Computer Software Products for Selecting Nucleic Acid Probes"; U.S. Patent Application Serial Number 10/006,174, filed December 4, 2001, and U.S. Patent Application Serial Number 10/027,682 (now abandoned), ~~attorney docket number 3440~~, filed December 21. 2001, and U.S. Patent Application Serial Number 10/028,884, ~~attorney docket number 3441~~, filed on December 21, 2001. All cited applications are incorporated herein by reference in their entireties for all purposes.

Please add at page 6, after line 15, the header "BRIEF DESCRIPTION OF THE DRAWINGS"

Please replace paragraph on page 7, line 16 with the following amended paragraph:

FIGURE 3 shows an exemplary computer network that is suitable for executing the computer software of the invention. A computer workstation 302 is connected with the application/data server(s) through a local area network (LAN) 301, such as Ethernet305. A printer 304 may be connected directly to the workstation or to the Ethernet 305. the LAN may be connected to a wide area network (WAN), such as the Internet 308, via a gateway server 307 which may also serve as a firewall between the WAN 308 and the LAN 305. In some embodiments, the workstation may communicate with outside data sources, such as the National Biotechnology Information Center, through the Internet. Various protocols, such as FTP and HTTP, may be used for data communication between the workstation and the outside data sources. Outside genetic data sources, such as the GenBank and the Center for Biotechnology Information (NCBI) can be found in the web site of NCBI (~~www.ncbi.nlm.nih.gov~~).

Please replace paragraph on page 11 line 15 with the following amended paragraph:

Microarray can be used in variety of ways. An exemplary microarray contains nucleic acids and is used to analyze nucleic acid samples. Typically, a nucleic acid sample is prepared from appropriate source and labeled with a signal moiety, such as a fluorescent label. The sample is hybridized with the array under appropriate conditions. The arrays are washed and otherwise processed to remove non-hybridized sample nucleic acids. The hybridization is then evaluated by detecting the distribution of the label on the chip. The distribution of the label may be detected by scanning the arrays to determine

fluorescence intensity distribution. Typically, the hybridization of each probe is reflected by several pixel intensities. The raw intensity data is stored ion a gray scale pixel intensity file. The GATC™ Consortium has specified several file formats for storing array intensity data. The final software specification is available on the website for GATC™ Consortium ~~at www.gatcconsortium.org and is incorporated herein by reference in its entirety~~. The pixel intensities are usually large. For example, a GATC™ compatible image file may be approximately 50 Mb if there are about 5000 pixels on each of the horizontal and vertical axes and if a two byte integer is used for every pixel intensity. The pixel may be grouped into cells (see GATC™ software specification). The probes in a cell are designed to have the same sequence (i.e., each cell is a probe area). A CEL file contains the statistics of a cell, e.g., the 75th percentile and standard deviation of intensities of pixel in a cell. The 50, 60, 70, 75 or 80th percentile of pixel intensity of a cell is often used as the intensity of the cell.